

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 19:03:02 ; Search time 32017 seconds  
(without alignments)  
3515.934 Million cell updates/sec

Title: US-10-049-743-1  
Perfect score: 3868  
Sequence: 1 gaattcgacagcgccg.....ggcttggtgacgagaattc 3868

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 630880

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

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- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_em.\*
- 5: gb\_ov.\*
- 6: gb\_ph.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_or.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pla.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	26	0.7	26	6	AR028693 Sequence
C 2	26	0.7	26	6	AR086504 Sequence
C 3	25	0.6	25	6	AR028694 Sequence
C 4	25	0.6	25	6	AR086505 Sequence
C 5	23	0.6	23	6	AR028695 Sequence
C 6	23	0.6	23	6	AR028696 Sequence
C 7	23	0.6	23	6	AR086506 Sequence
C 8	23	0.6	23	6	AR086507 Sequence
C 9	22	0.6	22	6	AR028698 Sequence
C 10	22	0.6	22	6	AR086509 Sequence
C 11	21	0.5	21	6	AR028691 Sequence
C 12	21	0.5	21	6	AR028692 Sequence
C 13	21	0.5	21	6	AR028699 Sequence
C 14	21	0.5	21	6	AR086502 Sequence
C 15	21	0.5	21	6	AR086503 Sequence
C 16	21	0.5	21	6	AR086510 Sequence
C 17	20	0.5	20	12	AB068351
C 18	20	0.5	30	6	AB6836
C 19	19.8	0.5	24	6	A75929
C 20	18.4	0.5	30	6	AB6832
C 21	18.2	0.5	30	6	AR117872
C 22	18	0.5	18	6	AR028700 Sequence
C 23	18	0.5	18	6	AR086511 Sequence
C 24	18	0.5	19	6	AR179243
C 25	18	0.5	27	6	AR143939
C 26	18	0.5	30	6	AX057066 Sequence
C 27	17.8	0.5	30	6	AX037190 Sequence
C 28	17.8	0.5	30	6	AX481912 Sequence
C 29	17.6	0.5	24	6	AX010291
C 30	17.6	0.5	25	6	A27144
C 31	17.4	0.4	28	6	AX040166 Sequence
C 32	17.4	0.4	28	6	AX356226 Sequence
C 33	17.4	0.4	29	6	E10625
C 34	17.4	0.4	29	6	E12084
C 35	17.4	0.4	30	6	AR099335 Sequence
C 36	17.4	0.4	30	6	AX037174 Sequence
C 37	17.4	0.4	30	6	AX105343
C 38	17.4	0.4	30	6	E30024
C 39	17.4	0.4	30	6	E30025
C 40	17.4	0.4	30	6	I28718
C 41	17.4	0.4	30	6	I28718 Sequence 21
C 42	17.2	0.4	24	6	AX443904 Sequence
C 43	17.2	0.4	25	6	AR144353
C 44	17.2	0.4	25	6	AX447880 Sequence
C 45	17.2	0.4	26	6	AR089201 Sequence

ALIGNMENTS

RESULT 1  
AR028693/c  
LOCUS AR028693  
DEFINITION Sequence 9 from patent US 5858753.  
ACCESSION AR028693  
VERSION AR028693.1 GI:5940666  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.  
TITLE Lipid kinase  
JOURNAL Patent: US 5858753-A 9 12-JAN-1999;  
FEATURES Location/Qualifiers

AR028693 26 bp DNA linear PAT 29-SEP-1999  
Sequence 9 from patent US 5858753.  
AR028693.1 GI:5940666

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QY 1500 GGAACGCTGCTCTACATGTGGGCC 1525
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Db 26 GGAACGCTGCTCTACATGTGGGCC 1

RESULT 2
AR086504/c 26 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 9 from patent US 5985589.
ACCESSION AR086504
VERSION AR086504.1 GI:10013270
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 26)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5985589-A 9 16-NOV-1999;
FEATURES
Location/Qualifiers
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Query Match 0.7%; Score 26; DB 6; Length 26;
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 GGAACGCTGCTCTACATGTGGGCC 1525
|||||
Db 26 GGAACGCTGCTCTACATGTGGGCC 1

RESULT 3
AR028694/c 25 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 10 from patent US 5858753.
ACCESSION AR028694
VERSION AR028694.1 GI:5940667
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 25)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5858753-A 10 12-JAN-1999;
FEATURES
Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.6e+06;
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QY 1435 GCGGACTGCCCATTCCTGGGCC 1459
|||||
Db 25 GCGGACTGCCCATTCCTGGGCC 1

RESULT 4
AR086505/c 25 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 10 from patent US 5985589.
ACCESSION AR086505
VERSION AR086505.1 GI:10013271
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 25)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5985589-A 10 16-NOV-1999;
FEATURES
Location/Qualifiers
source
1. .25
/organism="unknown"
BASE COUNT 4 a 9 c 10 g 2 t
ORIGIN

Query Match 0.6%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 GCGGACTGCCCATTCCTGGGCC 1

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LOCUS
DEFINITION Sequence 11 from patent US 5858753.
ACCESSION AR028695
VERSION AR028695.1 GI:5940668
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 23)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5858753-A 11 12-JAN-1999;
FEATURES
Location/Qualifiers
source
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BASE COUNT 4 a 6 c 10 g 3 t
ORIGIN

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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 CCCTGGAGCAGCGTTCGCCATC 1171
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Db 23 CCCTGGAGCAGCGTTCGCCATC 1

RESULT 6
AR028696/c 23 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 12 from patent US 5858753.
ACCESSION AR028696
VERSION AR028696.1 GI:5940669
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 23)
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5858753-A 12 12-JAN-1999;
FEATURES
Location/Qualifiers
source
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Db 1 CATGCTGACCTGCAGATGAT 21

RESULT 12  
AR028692/c 21 bp DNA linear PAT 29-SEP-1999  
LOCUS  
DEFINITION Sequence 8 from patent US 5858753.  
ACCESSION AR028692  
VERSION AR028692.1 GI:5940665  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.  
TITLE Lipid kinase  
JOURNAL Patent: US 5858753-A 8 12-JAN-1999;  
FEATURES Location/Qualifiers  
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BASE COUNT 4 a 9 c 4 g 4 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2899 CCGAGAGAGTGGCAGCTGTT 2919  
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Db 21 CCGAGAGAGTGGCAGCTGTT 1

RESULT 13  
AR028699/c 21 bp DNA linear PAT 29-SEP-1999  
LOCUS  
DEFINITION Sequence 16 from patent US 5858753.  
ACCESSION AR028699  
VERSION AR028699.1 GI:5940672  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.  
TITLE Lipid kinase  
JOURNAL Patent: US 5858753-A 16 12-JAN-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2712 TCAACAAGAGCAATGCGCAG 2732  
|||||  
Db 21 TCAACAAGAGCAATGCGCAG 1

RESULT 14  
AR086502 21 bp DNA linear PAT 07-SEP-2000  
LOCUS

DEFINITION Sequence 7 from patent US 5985589.  
ACCESSION AR086502  
VERSION AR086502.1 GI:10013268  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.  
TITLE Lipid kinase  
JOURNAL Patent: US 5985589-A 7 16-NOV-1999;  
FEATURES Location/Qualifiers  
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BASE COUNT 5 a 6 c 5 g 5 t  
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Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2557 CATGCTGACCTGCAGATGAT 2577  
|||||  
Db 1 CATGCTGACCTGCAGATGAT 21

RESULT 15  
AR086503/c 21 bp DNA linear PAT 07-SEP-2000  
LOCUS  
DEFINITION Sequence 8 from patent US 5985589.  
ACCESSION AR086503  
VERSION AR086503.1 GI:10013269  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.  
TITLE Lipid kinase  
JOURNAL Patent: US 5985589-A 8 16-NOV-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2899 CCGAGAGAGTGGCAGCTGTT 2919  
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Db 21 CCGAGAGAGTGGCAGCTGTT 1

Search completed: March 4, 2003, 05:06:16  
Job time : 32020 secs

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 19:00:52 ; Search time 739 Seconds  
(without alignments)  
11787.185 Million cell updates/sec

Title: US-10-049-743-1

Perfect score: 3868

Sequence: 1 gaattcgccagcagcgccg.....ggctctgggtacgagaattc 3868

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 1875172

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	26	0.7	26	19	AAV31345
C 2	26	0.7	26	20	AAV31345
C 3	26	0.7	26	21	AAV31345
C 4	25	0.6	25	19	AAV31346
C 5	25	0.6	25	20	AAV31346
C 6	25	0.6	25	21	AAV31346
C 7	23	0.6	23	19	AAV31347
C 8	23	0.6	23	20	AAV31348
C 9	23	0.6	23	21	AAV31349

C 10	23	0.6	23	20	AAV315940	Probe used to isol
C 11	23	0.6	23	21	AAV32889	Human PI 3-kinase-
C 12	23	0.6	23	21	AAV32890	Human PI 3-kinase-
C 13	22	0.6	22	19	AAV31350	Phosphatidylinositol
C 14	22	0.6	22	21	AAV315942	PCR primer used to
C 15	22	0.6	22	21	AAV32892	Human PI 3-kinase-
C 16	21.4	0.6	29	21	AAV31373	Polymorphic fragme
C 17	21	0.5	21	19	AAV31343	Phosphatidylinositol
C 18	21	0.5	21	19	AAV31344	Phosphatidylinositol
C 19	21	0.5	21	19	AAV31351	PCR primer used to
C 20	21	0.5	21	20	AAV315935	PCR primer used to
C 21	21	0.5	21	20	AAV315936	PCR primer used to
C 22	21	0.5	21	20	AAV315943	Human PI 3-kinase-
C 23	21	0.5	21	21	AAV31356	PCR primer for hum
C 24	21	0.5	21	21	AAV32885	Human PI 3-kinase-
C 25	21	0.5	21	21	AAV32886	Human PI 3-kinase-
C 26	21	0.5	21	21	AAV32893	Human PI 3-kinase-
C 27	20	0.5	20	21	AAV31114	PI3K antisense inh
C 28	20	0.5	20	21	AAV31115	PI3K antisense inh
C 29	20	0.5	20	21	AAV31116	PI3K antisense inh
C 30	20	0.5	20	21	AAV31117	PI3K antisense inh
C 31	20	0.5	20	21	AAV31118	PI3K antisense inh
C 32	20	0.5	20	21	AAV31119	PI3K antisense inh
C 33	20	0.5	20	21	AAV31120	PI3K antisense inh
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C 36	20	0.5	20	21	AAV31123	PI3K antisense inh
C 37	20	0.5	20	21	AAV31124	PI3K antisense inh
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C 41	20	0.5	20	21	AAV31128	PI3K antisense inh
C 42	20	0.5	20	21	AAV31129	PI3K antisense inh
C 43	20	0.5	20	21	AAV31130	PI3K antisense inh
C 44	20	0.5	20	21	AAV31131	PI3K antisense inh
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#### ALIGNMENTS

##### RESULT 1

AAV31345/C

ID AAV31345 standard; DNA; 26 BP.

AC AAV31345;

DT 12-OCT-1998 (first entry)

DE Phosphatidylinositol 3-kinase p110 delta subunit RACE primer.

XX Phosphatidylinositol 3-kinase; p110 delta; human; immune system;  
KW carcinogenesis; diagnosis; PCR; primer; RACE; ss.

OS Synthetic.

OS Homo sapiens.

PN WO9823760-A1.

XX 04-JUN-1998.

XX 25-NOV-1997; 97WO-US21655.

XX 25-NOV-1996; 96US-0777405.

XX (ICOS-) ICOS CORP.

XX Chantry DH, Hoekstra MF, Holtzman DA;

XX WPI; 1998-322735/28.

XX New phosphatidylinositol 3-kinase catalytic subunit - used to  
PT develop products for modulating kinase activity in immune system

PT signalling and in carcinogenesis  
 XX Example 1; Page 11; 53pp; English.  
 XX  
 CC 2 Antisense gene-specific oligonucleotide primers (see AAV31345 and  
 CC AAV31346) respectively comprise a primary RACE primer and a nested  
 CC RACE primer, and are based on the 5' end of M#928, a cDNA clone  
 CC obtained from human macrophage cDNA by PCR amplification (see  
 CC AAV31343-44). They were used to amplify 5' sequences of human  
 CC phosphatidylinositol 3-kinase (PI 3-kinase) p110 delta catalytic  
 CC subunit cDNA, using leucocyte cDNA as template. Amplified products  
 CC were used as templates in a nested PCR and the reamplified products  
 CC were then analysed using probes (see AAV31347-48) specific for p110  
 CC delta. The specific 5' RACE PCR products were combined with  
 CC partial clones #249 and M#928 to produce a composite cDNA (AAV31340)  
 CC sequence coding for human PI 3-kinase p110 delta catalytic subunit  
 CC (see AAV58570). This can be used to develop products for modulating  
 CC PI 3-kinase activity in immune system signalling and in  
 CC carcinogenesis.  
 XX  
 SQ Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;  
 Query Match 0.7%; Score 26; DB 19; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+04;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1500 GGAACGCTGCTCTACATGTGGCC 1525  
 Db 26 GGAACGCTGCTCTACATGTGGCC 1  
 RESULT 2  
 AAX15937/c  
 ID AAX15937 standard; DNA; 26 BP.  
 XX  
 AC AAX15937;  
 XX  
 DT 14-MAY-1999 (first entry)  
 XX  
 DE PCR primer used to amplify cDNA sequence encoding p110-delta.  
 XX  
 KW Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase;  
 KW PI3-kinase mediated signalling; immune system; phosphatidylinositol;  
 KW PI; kinase activity; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US5882910-A.  
 XX  
 PD 16-MAR-1999.  
 XX  
 PF 25-NOV-1997; 97US-0977871.  
 XX  
 PR 25-NOV-1997; 97US-0977871.  
 PR 25-NOV-1996; 96US-0777405.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Chantry DH, Hoekstra MF, Holtzman DA;  
 XX  
 DR WPI; 1999-214067/18.  
 XX  
 PT Novel catalytic subunits derived from phosphatidylinositol 3-kinase  
 PT enzymes - useful as antigens and for identifying agents which  
 PT modulate the enzymes kinase activity or binding to substrates and  
 PT co-factors  
 XX  
 XX Example 1; Columns 6; 22pp; English.  
 XX  
 CC PCR primers AAX15937-38 were used to isolate cDNA encoding a catalytic  
 CC subunit (p110-delta), derived from a phosphatidylinositol 3-kinase  
 CC enzyme which is involved in PI3-Kinase mediated signalling in the

CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),  
 CC and derivatives of it at the 3'-hydroxyl of the inositol ring).  
 CC p110-delta may be used as an antigen in the production of  
 CC antibodies (using standard techniques) which may be used, for  
 CC example, to modulate (ie blocking, inhibiting or stimulating) the  
 CC binding between p110-delta and its binding partner. p110-delta may  
 CC also be used in assays to identify modulators which inhibit or  
 CC activate its kinase activity.  
 XX

SQ Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;  
 Query Match 0.7%; Score 26; DB 20; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+04;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 26 GGAACGCTGCTCTACATGTGGCC 1

## RESULT 3

AAX32887/c

ID AAX32887 standard; DNA; 26 BP.

XX  
 AC AAX32887;

XX  
 DT 09-FEB-2000 (first entry)

XX  
 DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #9.  
 XX

KW Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;  
 KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;  
 KW phosphatidylinositol (3, 4, 5) triphosphate; PIP3; activation; G protein;  
 KW cellular response; growth; differentiation; apoptosis;  
 KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;  
 KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;  
 KW antagonist; agonist; treatment; disorder; cell growth;  
 KW cell differentiation; immune activation; PCR; primer; ss.  
 XX

OS Synthetic.

OS Homo sapiens.

XX  
 PN US5985589-A.

XX  
 PD 16-NOV-1999.

XX  
 PF 06-JAN-1999; 99US-0225951.

XX  
 PR 25-NOV-1997; 97US-0977871.

XX  
 PR 25-NOV-1996; 96US-0777405.

XX  
 PA (ICOS-) ICOS CORP.

XX  
 PI Holtzman DA, Hoekstra MF, Chantry DH;

XX  
 DR WPI; 2000-012785/01.

XX  
 PT Identifying modulators of lipid kinase subunit p110delta activity -

XX  
 PS Example 1; Column 6; 22pp; English.

XX  
 CC This sequence represents human p110-delta PCR primer #9, used in the  
 CC generation of a full-length cDNA (AAX32882) encoding a novel lipid  
 CC kinase catalytic subunit, p110-delta, related to phosphatidylinositol  
 CC 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a  
 CC membrane-localising p85 subunit and a catalytic p110 subunit. These  
 CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which  
 CC are differentially expressed, and p110 has to date three isoforms  
 CC (alpha, beta and gamma) that vary in their ability to associate with p85.  
 CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at  
 CC the 3' hydroxyl of the inositol ring with the primary product of PI  
 CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)  
 CC triphosphate (PIP3). PI 3-kinase is activated by interaction with G

CC proteins and PI 3-kinase activation is believed to be involved in a  
 CC range of cellular responses including cell growth, differentiation and  
 CC apoptosis. The downstream targets of the phosphorylated lipids generated  
 CC following PI 3-kinase activation have not been well characterised,  
 CC although some isoforms of protein kinase C (PKC) are directly activated  
 CC by PIP3 in vitro. PI 3-kinase also appears to be involved in certain  
 CC aspects of leukocyte activation, such as interleukin-2 (IL-2) production  
 CC in T cells, and leukocyte signalling through G-protein coupled  
 CC receptors. p110-delta, or nucleotides encoding it, may be used to  
 CC identify modulators of p110-delta and/or PI 3-kinase activity. These may  
 CC be useful in the treatment of disorders associated with cell growth,  
 CC cell differentiation, apoptosis or immune activation.

XX Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;

Query Match 0.7%; Score 26; DB 21; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+04;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 GGGACGCTGCCTCTACATGGGCC 1525

DB 26 GGGACGCTGCCTCTACATGGGCC 1

#### RESULT 4

AAV31346/C

ID AAV31346 standard; DNA; 25 BP.

XX AC AAV31346;

XX DT 12-OCT-1998 (first entry)

XX DE Phosphatidylinositol 3-kinase p110 delta subunit RACE primer.

XX KW Phosphatidylinositol 3-kinase; p110 delta; human; immune system;

XX KW carcinogenesis; diagnosis; PCR; primer; RACE; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN W09823760-A1.

XX PD 04-JUN-1998.

XX PF 25-NOV-1997; 97WO-US21655.

XX PR 25-NOV-1996; 96US-0777405.

XX PA (ICOS-) ICOS CORP.

XX PI Chantry DH, Hoekstra MF, Holtzman DA;

XX DR WPI; 1998-322736/28.

XX PT New phosphatidylinositol 3-kinase catalytic subunit - used to  
 develop products for modulating kinase activity in immune system  
 PT signalling and in carcinogenesis

XX PS Example 1; Page 11; 53pp; English.

XX CC 2 Antisense gene-specific oligonucleotide primers (see AAV31345 and  
 CC AAV31346) respectively comprise a primary RACE primer and a nested  
 CC RACE primer, and are based on the 5' end of M928, a cDNA clone  
 CC obtained from human macrophage cDNA by PCR amplification (see  
 CC AAV31343-44). They were used to amplify 5' sequences of human  
 CC phosphatidylinositol 3-kinase (PI 3-kinase) p110 delta catalytic  
 CC subunit cDNA, using leucocyte cDNA as template. Amplified products  
 CC were used as templates in a nested PCR and the reamplified products  
 CC were then analysed using probes (see AAV31347-48) specific for p110  
 CC delta. The specific 5' RACE PCR products were combined with  
 CC partial clones #249 and M928 to produce a composite cDNA (AAV31340)  
 CC sequence coding for human PI 3-kinase p110 delta catalytic subunit  
 CC (see AAW58570). This can be used to develop products for modulating

CC PI 3-kinase activity in immune system signalling and in  
 CC carcinogenesis.

XX Sequence 25 BP; 4 A; 9 C; 10 G; 2 T; 0 other;

Query Match 0.6%; Score 25; DB 19; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+04;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 GCGGACTGCCCCATTGCTGGGCC 1459

DB 25 GCGGACTGCCCCATTGCTGGGCC 1

#### RESULT 5

AAV15938/C

ID AAV15938 standard; DNA; 25 BP.

XX AC AAV15938;

XX DT 14-MAY-1999 (first entry)

XX DE PCR primer used to amplify cDNA sequence encoding p110-delta.

XX KW Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase;

XX KW PI3-Kinase mediated signalling; immune system; phosphatidylinositol;

XX KW PI; kinase activity; PCR primer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN US5882910-A.

XX PD 16-MAR-1999.

XX PF 25-NOV-1997; 97US-0977871.

XX PR 25-NOV-1997; 97US-0977871.

XX PR 25-NOV-1996; 96US-0777405.

XX PA (ICOS-) ICOS CORP.

XX PI Chantry DH, Hoekstra MF, Holtzman DA;

XX DR WPI; 1999-214067/18.

XX PT Novel catalytic subunits derived from phosphatidylinositol 3-kinase  
 PT enzymes - useful as antigens and for identifying agents which  
 PT modulate the enzymes kinase activity or binding to substrates and  
 PT co-factors

XX PS Example 1; Columns 6; 22pp; English.

XX CC PCR primers AAV15937-38 were used to isolate cDNA encoding a catalytic  
 CC subunit (p110-delta), derived from a Phosphatidylinositol 3-kinase  
 CC enzyme which is involved in PI3-Kinase mediated signalling in the  
 CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),  
 CC and derivatives of it at the 3'-hydroxyl of the inositol ring).  
 CC p110-delta may be used as an antigen in the production of  
 CC antibodies (using standard techniques) which may be used, for  
 CC example, to modulate (ie blocking, inhibiting or stimulating) the  
 CC binding between p110-delta and its binding partner. p110-delta may  
 CC also be used in assays to identify modulators which inhibit or  
 CC activate its kinase activity.

XX Sequence 25 BP; 4 A; 9 C; 10 G; 2 T; 0 other;

Query Match 0.6%; Score 25; DB 20; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+04;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 GCGGACTGCCCCATTGCTGGGCC 1459

|||||







```

PT modulate the enzymes kinase activity or binding to substrates and
PT co-factors
XX
PS Example 1; Columns 7; 22pp; English.
XX
CC Probes AX15939-40 were used to isolate cDNA encoding a catalytic
CC subunit (p110-delta), derived from a phosphatidylinositol 3-kinase
CC enzyme which is involved in PI3-Kinase mediated signalling in the
CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),
CC and derivatives of it at the 3'-hydroxyl of the inositol ring).
CC p110-delta may be used as an antigen in the production of
CC antibodies (using standard techniques) which may be used, for
CC example, to modulate (ie blocking, inhibiting or stimulating) the
CC binding between p110-delta and its binding partner. p110-delta may
CC also be used in assays to identify modulators which inhibit or
CC activate its kinase activity.
XX
SQ Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;
    Query Match          0.6%; Score 23; DB 20; Length 23;
    Best Local Similarity 100.0%; Pred. No. 1.4e+05;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 CTCGTGTCCTGTCGTGTCCTGG 1154
Db 23 CTCGTGTCCTGTCGTGTCCTGG 1

RESULT 11
AAZ32889/c
ID AAZ32889 standard; DNA; 23 BP.
XX
AC AAZ32889;
XX
DT 09-FEB-2000 (first entry)
DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #11.
XX
KW Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;
KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;
KW phosphatidylinositol (3, 4, 5) triphosphate; PIP3; activation; G protein;
KW cellular response; growth; differentiation; apoptosis;
KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;
KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;
KW antagonist; agonist; treatment; disorder; cell growth;
KW cell differentiation; immune activation; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5985589-A.
PD 16-NOV-1999.
XX
PF 06-JAN-1999; 98US-0225951.
XX
PR 25-NOV-1997; 97US-0977871.
PR 25-NOV-1996; 96US-0777405.
XX
PA (ICOS-) ICOS CORP.
XX
PI Holtzman DA, Hoekstra MF, Chantry DH;
XX
DR WPI; 2000-012785/01.
XX
PT Identifying modulators of lipid kinase subunit p110delta activity -
PS Example 1; Column 7; 22pp; English.
XX
CC This sequence represents human p110-delta PCR primer #11, used in the
CC generation of a full-length cDNA (AAZ32882) encoding a novel lipid
CC kinase catalytic subunit, p110-delta, related to phosphatidylinositol
CC 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a

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CC membrane-localising p85 subunit and a catalytic p110 subunit. These
CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which
CC are differentially expressed, and p110 has to date three isoforms
CC (alpha, beta and gamma) that vary in their ability to associate with p85.
CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at
CC the 3' hydroxyl of the inositol ring with the primary product of PI
CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)
CC triphosphate (PIP3). PI 3-kinase is activated by interaction with G
CC proteins and PI 3-kinase activation is believed to be involved in a
CC range of cellular responses including cell growth, differentiation and
CC apoptosis. The downstream targets of the phosphorylated lipids generated
CC following PI 3-kinase activation have not been well characterised,
CC although some isoforms of protein kinase C (PKC) are directly activated
CC by PIP3 in vitro. PI 3-kinase also appears to be involved in certain
CC aspects of leukocyte activation, such as interleukin-2 (IL-2) production
CC in T cells, and leukocyte signalling through G-protein coupled
CC receptors. p110-delta, or nucleotides encoding it, may be used to
CC identify modulators of p110-delta and/or PI 3-kinase activity. These may
CC be useful in the treatment of disorders associated with cell growth,
CC cell differentiation, apoptosis or immune activation.
XX
SQ Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other;
    Query Match          0.6%; Score 23; DB 21; Length 23;
    Best Local Similarity 100.0%; Pred. No. 1.4e+05;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 CCTGGAGCAGCGTTCGCGATC 1171
Db 23 CCTGGAGCAGCGTTCGCGATC 1

RESULT 12
AAZ32890/c
ID AAZ32890 standard; DNA; 23 BP.
XX
AC AAZ32890;
XX
DT 09-FEB-2000 (first entry)
DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #12.
XX
KW Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;
KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;
KW phosphatidylinositol (3, 4, 5) triphosphate; PIP3; activation; G protein;
KW cellular response; growth; differentiation; apoptosis;
KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;
KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;
KW antagonist; agonist; treatment; disorder; cell growth;
KW cell differentiation; immune activation; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5985589-A.
PD 16-NOV-1999.
XX
PF 06-JAN-1999; 99US-0225951.
XX
PR 25-NOV-1997; 97US-0977871.
PR 25-NOV-1996; 96US-0777405.
XX
PA (ICOS-) ICOS CORP.
XX
PI Holtzman DA, Hoekstra MF, Chantry DH;
XX
DR WPI; 2000-012785/01.
XX
PT Identifying modulators of lipid kinase subunit p110delta activity -
PS Example 1; Column 7; 22pp; English.
XX

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CC This sequence represents human p110-delta PCR primer #12, used in the  
 CC generation of a full-length cDNA (AA232882) encoding a novel lipid  
 CC kinase catalytic subunit, p110-delta, related to phosphatidylinositol  
 CC 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a  
 CC membrane-localising p85 subunit and a catalytic p110 subunit. These  
 CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which  
 CC are differentially expressed, and p110 has to date three isoforms  
 CC (alpha, beta and gamma) that vary in their ability to associate with p85.  
 CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at  
 CC the 3' hydroxyl of the inositol ring with the primary product of PI at  
 CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)  
 CC triphosphate (PIP3). PI 3-kinase is activated by interaction with G  
 CC proteins and PI 3-kinase activation is believed to be involved in a  
 CC range of cellular responses including cell growth, differentiation and  
 CC apoptosis. The downstream targets of the phosphorylated lipids generated  
 CC following PI 3-kinase activation have not been well characterised,  
 CC although some isoforms of protein kinase C (PKC) are directly activated  
 CC by PIP3 in vitro. PI 3-kinase also appears to be involved in certain  
 CC aspects of leukocyte activation, such as interleukin-2 (IL-2) production  
 CC in T cells, and leukocyte signalling through G-protein coupled  
 CC receptors. p110-delta, or nucleotides encoding it, may be used to  
 CC identify modulators of p110-delta and/or PI 3-kinase activity. These may  
 CC be useful in the treatment of disorders associated with cell growth,  
 CC cell differentiation, apoptosis or immune activation.

XX Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;

Query Match 0.6%; Score 23; DB 21; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 CTCCTGTGTCCTGTGTCCTGCG 1154

DB 23 CTCCTGTGTCCTGTGTCCTGCG 1

RESULT 13

AAV31350/c

ID AAV31350 standard; DNA; 22 BP.

XX AAV31350;

XX 12-OCT-1998 (first entry)

XX Phosphatidylinositol 3-kinase p110 delta subunit primer.

DE Phosphatidylinositol 3-kinase; p110 delta; human; immune system;  
 KW carcinogenesis; diagnosis; PCR; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9823760-A1.

XX 04-JUN-1998.

XX 25-NOV-1997; 97WO-US21655.

XX 25-NOV-1996; 96US-0777405.

XX (ICOS-) ICOS CORP.

XX Chantry DH, Hoekstra MF, Holtzman DA;

XX WPI; 1998-322736/28.

XX New phosphatidylinositol 3-kinase catalytic subunit - used to  
 PT develop products for modulating kinase activity in immune system  
 PT signalling and in carcinogenesis

XX Example 1; Page 12; 53pp; English.

XX This 3' primer was used with a 5' primer (see AAV31349) in the PCR

CC amplification of 5'RACE PCR products (see AAV31345-46) of human  
 CC leukocyte cDNA. The 5' primer includes a 5' BamHI site and  
 CC sequences that code for a FLAG peptide (see AAW58571) which is  
 CC recognised by the M2 anti-FLAG monoclonal antibody. The PCR  
 CC product was combined with restriction fragments of partial clones  
 CC #249 and M#928 to produce a full-length cDNA (see AAV31347) for the  
 CC p100 delta catalytic subunit (see AAW58570) of human  
 CC phosphatidylinositol 3-kinase (PI 3-kinase). This was incorporated  
 CC into expression vector pcDNA3, and FLAG-tagged p110 delta was  
 CC expressed in transfected COS cells. p110 delta can be used to  
 CC develop products for modulating PI 3-kinase activity in immune  
 CC system signalling and in carcinogenesis.

XX Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;

Query Match 0.6%; Score 22; DB 19; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1501 GGAACGCTGCCTCTACATGTGG 1522

DB 22 GGAACGCTGCCTCTACATGTGG 1

RESULT 14

AAV15942/c

ID AAV15942 standard; DNA; 22 BP.

XX AAV15942;

XX 14-MAY-1999 (first entry)

XX PCR primer used to amplify cDNA sequence encoding p110-delta.

DE Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase;

KW PI3-Kinase mediated signalling; immune system; phosphatidylinositol;

KW PI; kinase activity; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX US5882910-A.

XX 16-MAR-1999.

XX 25-NOV-1997; 97US-0977871.

XX 25-NOV-1997; 97US-0977871.

XX 25-NOV-1996; 96US-0777405.

XX (ICOS-) ICOS CORP.

XX Chantry DH, Hoekstra MF, Holtzman DA;

XX WPI; 1999-214067/18.

XX Novel catalytic subunits derived from phosphatidylinositol 3-kinase  
 PT enzymes - useful as antigens and for identifying agents which  
 PT modulate the enzymes kinase activity or binding to substrates and  
 PT co-factors

XX Example 1; Columns 7; 22pp; English.

XX PCR primers AAV15941-42 were used to isolate cDNA encoding a catalytic  
 CC subunit (p110-delta), derived from a Phosphatidylinositol 3-kinase  
 CC enzyme which is involved in PI3-Kinase mediated signalling in the  
 CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),  
 CC and derivatives of it at the 3'-hydroxyl of the inositol ring).

CC p110-delta may be used as an antigen in the production of

CC antibodies (using standard techniques) which may be used, for

CC example, to modulate (ie blocking, inhibiting or stimulating) the

CC binding between p110-delta and its binding partner. p110-delta may

CC also be used in assays to identify modulators which inhibit or

CC activate its kinase activity.  
XX  
SQ Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;  
Query Match 0.6%; Score 22; DB 20; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1501 GGAACGCTGCCTCTACATGTGG 1522  
Db 22 GGAACGCTGCCTCTACATGTGG 1  
RESULT 15  
ID AA232892/c  
XX AA232892 standard; DNA; 22 BP.  
AC AA232892;  
XX  
DT 09-FEB-2000 (first entry)  
XX  
DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #14.  
XX  
KW Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;  
KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;  
KW phosphatidylinositol (3, 4, 5) triphosphate; PI3; activation; G protein;  
KW cellular response; growth; differentiation; apoptosis;  
KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;  
KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;  
KW antagonist; agonist; treatment; disorder; cell growth;  
KW cell differentiation; immune activation; PCR; primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US5985589-A.  
XX 16-NOV-1999.  
PD  
XX  
PF 06-JAN-1999; 99US-0225951.  
XX  
XX 25-NOV-1997; 97US-0977871.  
PR 25-NOV-1996; 96US-0777405.  
XX  
PA (ICOS-) ICOS CORP.  
XX  
XX Holtzman DA, Hoekstra MF, Chantry DH;  
XX  
DR WPI; 2000-012785/01.  
XX  
PT Identifying modulators of lipid kinase subunit p110delta activity -  
XX  
PS Example 1; Column 7; 22pp; English.  
XX  
CC This sequence represents human p110-delta PCR primer #14, used in the  
CC generation of a full-length cDNA (AA232882) encoding a novel lipid  
CC kinase catalytic subunit, p110-delta, related to phosphatidylinositol  
CC 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a  
CC membrane-localising p85 subunit and a catalytic p110 subunit. These  
CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which  
CC are differentially expressed, and p110 has to date three isoforms  
CC (alpha, beta and gamma) that vary in their ability to associate with p85.  
CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at  
CC the 3' hydroxyl of the inositol ring with the primary product of PI  
CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)  
CC triphosphate (PIP3). PI 3-kinase is activated by interaction with G  
CC proteins and PI 3-kinase activation is believed to be involved in a  
CC range of cellular responses including cell growth, differentiation and  
CC apoptosis. The downstream targets of the phosphorylated lipids generated  
CC following PI 3-kinase activation have not been well characterised,  
CC although some isoforms of protein kinase C (PKC) are directly activated  
CC by PIP3 in vitro. PI 3-kinase also appears to be involved in certain  
CC aspects of leukocyte activation, such as interleukin-2 (IL-2) production

CC in T cells, and leukocyte signalling through G-protein coupled  
CC receptors, p110-delta, or nucleotides encoding it, may be used to  
CC identify modulators of p110-delta and/or PI 3-kinase activity. These may  
CC be useful in the treatment of disorders associated with cell growth,  
CC cell differentiation, apoptosis or immune activation.  
XX  
SQ Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;  
Query Match 0.6%; Score 22; DB 21; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1501 GGAACGCTGCCTCTACATGTGG 1522  
Db 22 GGAACGCTGCCTCTACATGTGG 1  
Search completed: March 3, 2003, 20:12:24  
Job time : 741 secs

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 19:58:31 ; Search time 135 Seconds  
(without alignments)  
8786.857 Million cell updates/sec

Title: US-10-049-743-1  
Perfect score: 3868  
Sequence: 1 gaattcgacagcgccg.....ggtcttggtacagaattc 3868

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues  
Total number of hits satisfying chosen parameters: 452144

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
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2: /cgn2.6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2.6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2.6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2.6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	26	0.7	26	2	US-08-777-405A-9
C 2	26	0.7	26	2	US-08-977-871A-9
C 3	26	0.7	26	2	US-09-225-951-9
C 4	25	0.6	25	2	US-08-777-405A-10
C 5	25	0.6	25	2	US-08-977-871A-10
C 6	25	0.6	25	2	US-09-225-951-10
C 7	23	0.6	23	2	US-08-777-405A-11
C 8	23	0.6	23	2	US-08-777-405A-12
C 9	23	0.6	23	2	US-08-977-871A-11
C 10	23	0.6	23	2	US-08-977-871A-12
C 11	23	0.6	23	2	US-09-225-951-11
C 12	23	0.6	23	2	US-09-225-951-12
C 13	22	0.6	22	2	US-08-777-405A-14
C 14	22	0.6	22	2	US-08-977-871A-14
C 15	22	0.6	22	2	US-09-225-951-14
C 16	21	0.5	21	2	US-08-777-405A-7
C 17	21	0.5	21	2	US-08-777-405A-8
C 18	21	0.5	21	2	US-08-777-405A-16
C 19	21	0.5	21	2	US-08-977-871A-7
C 20	21	0.5	21	2	US-08-977-871A-8
C 21	21	0.5	21	2	US-08-977-871A-16
C 22	21	0.5	21	2	US-09-225-951-7
C 23	21	0.5	21	2	US-09-225-951-8
C 24	21	0.5	21	2	US-09-225-951-16
C 25	21	0.5	21	3	US-09-357-070-3
C 26	20	0.5	20	3	US-09-357-070-8
C 27	20	0.5	20	3	US-09-357-070-9

C 28	20	0.5	20	3	US-09-357-070-10	Sequence 10, Appl
C 29	20	0.5	20	3	US-09-357-070-11	Sequence 11, Appl
C 30	20	0.5	20	3	US-09-357-070-12	Sequence 12, Appl
C 31	20	0.5	20	3	US-09-357-070-13	Sequence 13, Appl
C 32	20	0.5	20	3	US-09-357-070-14	Sequence 14, Appl
C 33	20	0.5	20	3	US-09-357-070-15	Sequence 15, Appl
C 34	20	0.5	20	3	US-09-357-070-16	Sequence 16, Appl
C 35	20	0.5	20	3	US-09-357-070-17	Sequence 17, Appl
C 36	20	0.5	20	3	US-09-357-070-18	Sequence 18, Appl
C 37	20	0.5	20	3	US-09-357-070-19	Sequence 19, Appl
C 38	20	0.5	20	3	US-09-357-070-20	Sequence 20, Appl
C 39	20	0.5	20	3	US-09-357-070-21	Sequence 21, Appl
C 40	20	0.5	20	3	US-09-357-070-22	Sequence 22, Appl
C 41	20	0.5	20	3	US-09-357-070-23	Sequence 23, Appl
C 42	20	0.5	20	3	US-09-357-070-24	Sequence 24, Appl
C 43	20	0.5	20	3	US-09-357-070-25	Sequence 25, Appl
C 44	20	0.5	20	3	US-09-357-070-26	Sequence 26, Appl
C 45	20	0.5	20	3	US-09-357-070-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1  
US-08-777-405A-9/C  
; Sequence 9, Application US/08777405A  
; Patent No. 5858753  
; GENERAL INFORMATION:  
; APPLICANT: Chantry, David  
; APPLICANT: Hoekstra, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: No. 5858753el Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
; STREET: 6300 Sears Tower/233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/777,405A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5858753and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33441  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-777-405A-9

Query Match 0.7%; Score 26; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1500 GGGACGCTGCTTACATGTGGCCC 1525

Db 26 GGGACGCTGCTTACATGTGGCCC 1

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RESULT 2
US-08-977-871A-9/c
; Sequence 9, Application US/08977871A
; Patent No. 5882910
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5882910el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,871A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/777,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-977-871A-9
Query Match 0.7%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1500 GGAACGCTGCCTCATGTGGCC 1525
Db 26 GGAACGCTGCCTCATGTGGCC 1

RESULT 3
US-09-225-951-9/c
; Sequence 9, Application US/09225951
; Patent No. 5985589
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5985589el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
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; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,951
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5985589and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-09-225-951-9
Query Match 0.7%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1500 GGAACGCTGCCTCATGTGGCC 1525
Db 26 GGAACGCTGCCTCATGTGGCC 1

RESULT 4
US-08-777-405A-10/c
; Sequence 10, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5858753el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5858753and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-777-405A-10

Query Match
Best Local Similarity 0.6%; Score 25; DB 2; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 GCGGACTGCCCATTCCTGGGCC 1459
|||||
Db 25 GCGGACTGCCCATTCCTGGGCC 1

RESULT 5
US-08-977-871A-10/c
; Sequence 10, Application US/08977871A
; Patent No. 5882910
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; TITLE OF INVENTION: No. 5882910el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,871A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/777,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-977-871A-10

Query Match
Best Local Similarity 0.6%; Score 25; DB 2; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 GCGGACTGCCCATTCCTGGGCC 1459
|||||
Db 25 GCGGACTGCCCATTCCTGGGCC 1

RESULT 6
US-09-225-951-10/c
; Sequence 10, Application US/09225951
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; Patent No. 5985589
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5985589el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,951
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5985589and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-225-951-10

Query Match
Best Local Similarity 0.6%; Score 25; DB 2; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 GCGGACTGCCCATTCCTGGGCC 1459
|||||
Db 25 GCGGACTGCCCATTCCTGGGCC 1

RESULT 7
US-08-777-405A-11/c
; Sequence 11, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5858753el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405A
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;; FILING DATE: 435  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: No. 5858753and, Greta E.  
;; REGISTRATION NUMBER: 35,302  
;; REFERENCE/DOCKET NUMBER: 27866/33441  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (312) 474-6300  
;; TELEFAX: (312) 474-0448  
;; TELEX: 25-3856  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 23 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: other nucleic acid  
US-08-777-405A-11

Query Match 0.6%; Score 23; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 CCTGGAGCAGCGTTCGCATC 1171  
|||||  
DB 23 CCTGGAGCAGCGTTCGCATC 1

RESULT 8  
US-08-777-405A-12/c  
; Sequence 12, Application US/08777405A  
; Patent No. 5858753  
; GENERAL INFORMATION:  
; APPLICANT: Chantry, David  
; APPLICANT: Hoekstra, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: No. 5858753el Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
; STREET: 6300 Sears Tower/233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,405A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5858753and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33441  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
US-08-777-405A-12

Query Match 0.6%; Score 23; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1132 CTCTGTGTCCTGTGTGGTCCCTGG 1154  
|||||  
DB 23 CTCTGTGTCCTGTGTGGTCCCTGG 1

RESULT 9  
US-08-977-871A-11/c  
; Sequence 11, Application US/08977871A  
; Patent No. 5882910  
; GENERAL INFORMATION:  
; APPLICANT: Chantry, David  
; APPLICANT: Hoekstra, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: No. 5882910el Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
; STREET: 6300 Sears Tower/233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/977,871A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/777,405  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5882910and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33441  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
US-08-977-871A-11

Query Match 0.6%; Score 23; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 CCTGGAGCAGCGTTCGCATC 1171  
|||||  
DB 23 CCTGGAGCAGCGTTCGCATC 1

RESULT 10  
US-08-977-871A-12/c  
; Sequence 12, Application US/08977871A  
; Patent No. 5882910  
; GENERAL INFORMATION:  
; APPLICANT: Chantry, David  
; APPLICANT: Hoekstra, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: No. 5882910el Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:



```
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,871A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/777,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-977-871A-12

Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 CTCGTGTCCTGTGGTCCCTGG 1154
DB 23 CTCGTGTCCTGTGGTCCCTGG 1

RESULT 11
US-09-225-951-11/c
; Sequence 11, Application US/09225951
; Patent No. 5985589
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5985589el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,951
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5985589and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-09-225-951-11
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; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-09-225-951-11

Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 CCTGGAGCAGCGGTCCTCCGCATC 1171
DB 23 CCTGGAGCAGCGGTCCTCCGCATC 1

RESULT 12
US-09-225-951-12/c
; Sequence 12, Application US/09225951
; Patent No. 5985589
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5985589el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,951
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5985589and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-09-225-951-12

Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 CTCGTGTCCTGTGGTCCCTGG 1154
DB 23 CTCGTGTCCTGTGGTCCCTGG 1
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; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
US-09-225-951-14

Query Match 0.6%; Score 22; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1501 GGAACGCTGCCTCTACATGTGG 1522  
|||||  
Db 22 GGAACGCTGCCTCTACATGTGG 1

Search completed: March 4, 2003, 06:27:43  
Job time : 136 secs



GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 20:00:22 ; Search time 1105 Seconds  
(without alignments)  
2338.022 Million cell updates/sec

Title: US-10-049-743-1  
Perfect score: 3868  
Sequence: 1 gaattcgccagcgccgcg.....ggcttgggtacgagaattc 3868

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 478924 seqs, 33395956 residues  
Total number of hits satisfying chosen parameters: 200426

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PublishedApplications.NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
c 1	20	0.5	30	US-09-494-438-1
c 2	18.6	0.5	29	US-09-596-606-4
c 3	17.6	0.5	25	US-09-866-108-3779
c 4	17.6	0.5	25	US-09-866-108-3780
c 5	17.4	0.4	28	US-09-894-633A-20
c 6	17.4	0.4	30	US-09-791-171-160
c 7	17.2	0.4	22	US-09-804-171A-16
c 8	17	0.4	25	US-09-866-108-3764
c 9	17	0.4	25	US-09-866-108-3778
c 10	17	0.4	25	US-09-866-108-3895
c 11	17	0.4	25	US-09-866-108-3945
c 12	17	0.4	25	US-09-866-108-4394
c 13	17	0.4	25	US-09-866-108-4395
c 14	17	0.4	25	US-09-866-108-12035
c 15	17	0.4	25	US-09-866-108-12894
c 16	17	0.4	25	US-09-866-108-12896
c 17	17	0.4	25	US-09-866-108-12897
c 18	17	0.4	25	US-09-866-108-12898
c 19	17	0.4	25	US-09-866-108-12899

20	17	0.4	25	10	US-09-866-108-12944	Sequence 12944, A
21	17	0.4	25	10	US-09-866-108-12985	Sequence 12985, A
c 22	17	0.4	25	10	US-09-866-108-13772	Sequence 13772, A
c 23	17	0.4	25	10	US-09-866-108-14859	Sequence 14859, A
c 24	17	0.4	26	9	US-09-785-548-19	Sequence 19, Appl
c 25	17	0.4	26	10	US-09-918-203-4	Sequence 4, Appl
c 26	17	0.4	30	9	US-09-729-658B-45	Sequence 45, Appl
c 27	16.8	0.4	24	10	US-09-811-259-6	Sequence 6, Appl
c 28	16.8	0.4	25	10	US-09-866-108-3896	Sequence 3896, Ap
c 29	16.8	0.4	25	10	US-09-866-108-3897	Sequence 3897, Ap
c 30	16.8	0.4	25	10	US-09-866-108-3898	Sequence 3898, Ap
c 31	16.8	0.4	25	10	US-09-866-108-3899	Sequence 3899, Ap
c 32	16.8	0.4	25	10	US-09-866-108-3900	Sequence 3900, Ap
c 33	16.8	0.4	29	9	US-09-941-492-2	Sequence 2, Appl
c 34	16.8	0.4	29	9	US-09-941-492-19	Sequence 19, Appl
c 35	16.8	0.4	29	10	US-09-852-000-4	Sequence 4, Appl
c 36	16.8	0.4	29	10	US-09-852-000-5	Sequence 5, Appl
c 37	16.8	0.4	29	10	US-09-756-095-2	Sequence 2, Appl
c 38	16.8	0.4	29	10	US-09-756-095-19	Sequence 19, Appl
c 39	16.6	0.4	24	9	US-10-037-667-13	Sequence 13, Appl
c 40	16.6	0.4	25	10	US-09-866-108-3760	Sequence 3760, Ap
c 41	16.6	0.4	25	10	US-09-866-108-3761	Sequence 3761, Ap
c 42	16.6	0.4	25	10	US-09-866-108-3762	Sequence 3762, Ap
c 43	16.6	0.4	25	10	US-09-866-108-3781	Sequence 3781, Ap
c 44	16.6	0.4	25	10	US-09-866-108-3943	Sequence 3943, Ap
c 45	16.6	0.4	25	10	US-09-866-108-3944	Sequence 3944, Ap

ALIGNMENTS

RESULT 1  
US-09-494-438-1/c  
; Sequence 1, Application US/09494438  
; Patent No. US20020037504A1  
; GENERAL INFORMATION:  
; APPLICANT: ARAHIRA, MASAOMI  
; APPLICANT: FUKUZAWA, CHIKAFUSA  
; TITLE OF INVENTION: METHOD FOR PREPARING TEMPLATE DNA FROM PROCESSED  
; TITLE OF INVENTION: VEGETABLE FOOD, WHICH IS FEASIBLE FOR AMPLIFICATION OF  
; FILE REFERENCE: 8361-0011-0  
; CURRENT APPLICATION NUMBER: US/09/494,438  
; CURRENT FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: JP336142/1999  
; PRIOR FILING DATE: 1999-11-26  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
US-09-494-438-1

Query Match 0.5%; Score 20; DB 10; Length 30;  
Best Local Similarity 82.1%; Pred. No. 8.3e+04;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2688 CAGACACCATCGCCAACTCAACTCAA 2715

DB 28 CTGACACCATCCCGAGATCCACACAA 1

RESULT 2

US-09-996-606-4/c  
; Sequence 4, Application US/09996606  
; Patent No. US20020127653A1  
; GENERAL INFORMATION:  
; APPLICANT: SOPEET, DANIEL R.  
; RUBEN, STEVEN M.  
; TITLE OF INVENTION: HEMATOPOIETIC SIGNALING FACTOR

NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: US  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/996,606  
FILING DATE: 30-Nov-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/008,490  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0600001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-996-606-4

Query Match 0.5%; Score 18.6; DB 10; Length 29;  
Best Local Similarity 84.0%; Pred. No. 1.7e+05;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3356 AGAGGAGCGGCTCGGGTGGTGG 3380  
||| ||||| ||||| ||||| ||  
DB 27 AGTGGAGCGCGCGGTCGACGG 3

## RESULT 3

US-09-866-108-3779  
; Sequence 3779, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 3779  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-3779

Query Match 0.5%; Score 17.6; DB 10; Length 25;  
Best Local Similarity 83.3%; Pred. No. 2.8e+05;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2322 CCCAGACCAAGGAGCTGATGCAC 2345  
||||| ||||| ||||| |||||  
DB 2 CCCAGGCCAAGGAACGTGGC 25

## RESULT 4

US-09-866-108-3780  
; Sequence 3780, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 3780  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-3780

Query Match 0.5%; Score 17.6; DB 10; Length 25;  
Best Local Similarity 83.3%; Pred. No. 2.8e+05;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2322 CCCAGACCAAGGAGCTGATGCAC 2345  
||||| ||||| ||| |||||  
Db 1 CCCAGGCCAAGGAAGCTGGCACT 24

RESULT 5  
US-09-894-633A-20/c  
; Sequence 20, Application US/09894633A  
; Patent No. US20020124285A1  
; GENERAL INFORMATION:  
; APPLICANT: Conner, Timothy  
; APPLICANT: Dubois, Patrice  
; APPLICANT: Malven, Marianne  
; APPLICANT: Masucci, James  
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRESSION  
; FILE REFERENCE: 38-21(15856)B  
; CURRENT APPLICATION NUMBER: US/09/894,633A  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 60/214,357  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 09/894,633  
; PRIOR FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 20  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(28)  
; OTHER INFORMATION: synthetic primer sequence  
US-09-894-633A-20

Query Match 0.4%; Score 17.4; DB 10; Length 28;  
Best Local Similarity 77.8%; Pred. No. 3.3e+05;  
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1587 ACACGGATAGCCGCGCTCCCTGTCTCA 1613  
||| ||| ||||| |||||  
Db 27 ACAGGGACCGCGCGCTCCCTGTCTCA 1

RESULT 6  
US-09-791-171-160  
; Sequence 160, Application US/09791171  
; Patent No. US20020094336A1  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSEN, Peter  
; APPLICANT: NIELSEN, Rikke  
; APPLICANT: OETTINGER, Thomas  
; APPLICANT: RASMUSSEN, Peter Birk

; APPLICANT: ROSENKRANDS, Ida  
; APPLICANT: WELDLINGH, Karin  
; APPLICANT: FLORIO, Walter  
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS  
; FILE REFERENCE: 670001-2002.1  
; CURRENT APPLICATION NUMBER: US/09/791,171  
; CURRENT FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 09/050,739  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 0376/97  
; PRIOR FILING DATE: 1997-04-02  
; PRIOR APPLICATION NUMBER: 1277/97  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/044,624  
; PRIOR FILING DATE: 1997-04-18  
; PRIOR APPLICATION NUMBER: 60/070,488  
; PRIOR FILING DATE: 1998-01-05  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 160  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-09-791-171-160

Query Match 0.4%; Score 17.4; DB 10; Length 30;  
Best Local Similarity 77.8%; Pred. No. 3.4e+05;  
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3268 TGAGAGCTGGAAACCAAGTGAAC 3294  
||||| ||| ||| ||| ||| |||  
Db 2 TGAGATCTAGATGCCACAGGGAAC 28

RESULT 7  
US-09-804-717A-16  
; Sequence 16, Application US/09804717A  
; Patent No. US20020164311A1  
; GENERAL INFORMATION:  
; APPLICANT: Strom, Terry B.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR PREVENTION OF GRAFT REJECTION  
; FILE REFERENCE: 01948-051003  
; CURRENT APPLICATION NUMBER: US/09/804,717A  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: US 09/304,755  
; PRIOR FILING DATE: 1999-05-04  
; PRIOR APPLICATION NUMBER: US 08/273,402  
; PRIOR FILING DATE: 1994-07-11  
; PRIOR APPLICATION NUMBER: US 08/024,569  
; PRIOR FILING DATE: 1993-03-01  
; PRIOR APPLICATION NUMBER: US 07/843,731  
; PRIOR FILING DATE: 1992-02-28  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-804-717A-16

Query Match 0.4%; Score 17.2; DB 9; Length 22;  
Best Local Similarity 86.4%; Pred. No. 3.3e+05;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 878 TTCCGGCAGCGGTGTGTGGACC 899  
||||| ||| ||||| |||  
Db 1 TTCCGGCAACAGCTGTGTGGACC 22

RESULT 8  
US-09-866-108-3764

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; Sequence 3764, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 3764
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-3764
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Query Match 0.4%; Score 17; DB 10; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3367 CTGCGGTCGTGGGACCAAGCACA 3391
Db 1 CTGGGGGCTCTTGGGACCAAGCACA 25
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RESULT 9
US-09-866-108-3778
; Sequence 3778, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
```

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; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR APPLICATION NUMBER: PCT/US01/00669
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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 3778
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-3778
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Query Match 0.4%; Score 17; DB 10; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2320 GCCCAGACCAAGGAGCTGATGCAC 2344
Db 1 GACCCAGGCCAAGGAGCTGATGCAC 25
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RESULT 10
US-09-866-108-3895/C
; Sequence 3895, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
```



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; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-3895
```

```
Query Match 0.4%; Score 17; DB 10; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy 727 CTGGGGCGCTGCTACCTCGGCGTC 751
Db 25 CTGGGGCGCTGCTCCCTGCTGTC 1
```

```
RESULT 11
US-09-866-108-3945
; Sequence 3945, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
```

```
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3945
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-3945
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Query Match 0.4%; Score 17; DB 10; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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```
Qy 3205 ACTGGGAAACACAGAGGAGGCA 3229
Db 1 ACCAGGAAAGCAGAGGAGGGA 25
```

```
RESULT 12
US-09-866-108-4394
; Sequence 4394, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
```

```

Query Match      0.4%; Score 17; DB 10; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1792 GAAGTCGCGCATGAAGTCCAGG 1816
      ||||| ||||| ||||| |||||
Db 1 GAAGTTGCGGAATGAATCCGCG 25

```

```
RESULT 15
US-09-866-108-12894
; Sequence 12894: Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 12894
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-12894

Query Match          0.4%; Score 17; DB 10; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Caps 0;

QY 323 AGCACCATCAAGCAGCTGCTGTGGC 347
Db 1 AACACCATCAAGCAGCTGGAGCAGC 25

Search completed: March 4, 2003, 06:46:21
Job time : 1106 secs
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GenCore version 5.1.4\_b5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 19:51:57 ; Search time 4726 Seconds  
(without alignments)  
13255.214 Million cell updates/sec

Title: US-10-049-743-1  
Perfect score: 3868  
Sequence: 1 gaattcgccagcagcgccg.....ggtcttggtacgagaattc 3868

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 30108  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_fod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.6	0.5	28	14	T47368
2	18.6	0.5	30	13	BM399411
3	18	0.5	28	9	AL584657
c 4	17	0.4	29	17	BH861248
c 5	16.8	0.4	26	17	AZ479681
6	16.8	0.4	26	17	AZ780072

c	7	16.8	0.4	28	9	AA973948
	8	16.8	0.4	30	13	BM398517
	9	16.6	0.4	30	13	BM398517
c	10	16.4	0.4	29	17	AZ404206
	11	16.4	0.4	29	17	AZ789420
	12	16.4	0.4	30	17	AZ840149
c	13	16.2	0.4	22	9	AA953755
	14	16.2	0.4	30	13	BM398127
c	15	16.2	0.4	30	13	AZ343274
	16	16.2	0.4	30	17	AZ601864
c	17	16	0.4	25	9	AA766400
	18	16	0.4	27	17	TA212C03P
	19	16	0.4	28	17	AZ371129
	20	16	0.4	30	17	AZ343274
c	21	15.8	0.4	23	17	AZ408639
	22	15.8	0.4	28	17	AZ818371
	23	15.8	0.4	28	17	AZ345640
	24	15.8	0.4	28	17	AZ502451
c	25	15.8	0.4	29	9	AU269375
	26	15.8	0.4	29	14	D45817
c	27	15.8	0.4	30	10	AV852654
	28	15.8	0.4	30	14	H41620
c	29	15.8	0.4	30	17	BH810436
c	30	15.6	0.4	24	17	AZ308159
c	31	15.6	0.4	24	17	AZ779573
c	32	15.6	0.4	27	13	BM401118
c	33	15.6	0.4	29	17	AZ315608
c	34	15.6	0.4	29	17	AZ476559
c	35	15.4	0.4	26	17	AZ308069
c	36	15.4	0.4	27	17	AZ345323
c	37	15.4	0.4	27	17	AZ404206
c	38	15.4	0.4	28	9	AI006312
c	39	15.4	0.4	29	17	AZ803680
c	40	15.4	0.4	30	17	AZ80802
c	41	15.4	0.4	30	17	AZ822508
c	42	15.2	0.4	20	17	AZ7844682
c	43	15.2	0.4	22	17	AZ942905
c	44	15.2	0.4	28	9	AI625245
c	45	15.2	0.4	28	9	AI697335

ALIGNMENTS

RESULT 1  
T47368  
LOCUS  
DEFINITION  
IMAGE:71023 5' similar to gb:J02683 ADP,ATP CARRIER  
PROTEIN, FIBROBLAST ISOFORM (HUMAN), mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT

T47368 28 bp mRNA linear EST 01-FEB-1995  
yb13b04.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone  
IMAGE:71023 5' similar to gb:J02683 ADP,ATP CARRIER  
PROTEIN, FIBROBLAST ISOFORM (HUMAN), mRNA sequence.  
T47368  
T47368.1 GI:649349  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 28)  
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,  
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins  
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore  
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,  
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,  
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
97044478  
Other\_ESTs: yb13b04.s1  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 89

High quality sequence starts: 1 High quality sequence stops: 1  
Source: IMAGE Consortium, LNL This clone is available royalty-free  
through LNL; contact the IMAGE Consortium (info@image.lnl.gov)  
for further information. Trace considered overall poor quality  
Insert length: 89 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

Location/Qualifiers

#### FEATURES

source

1. .28  
/organism="Homo sapiens"  
/db\_xref="GDB:491920"  
/db\_xref="taxon:9606"  
/clone="IMAGE:71023"  
/clone\_lib="Stratagene placenta (#937225)"  
/sex="male"  
/lab\_host="SOLR cells (kanamycin resistant)"  
/note="Organ: placenta; Vector: pBluescript SK-; Site:1:  
EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer:  
Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP  
XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGG 3' -3'  
adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'

#### BASE COUNT

4 a 7 c 11 g 6 t

#### ORIGIN

Query Match 0.5%; Score 19.6; DB 14; Length 28;  
Best Local Similarity 84.6%; Pred. No. 3.4e+06;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1204 CGAGCGGATGAAGCTGGTGGTGCAGG 1229  
||||||| 1 ||||| 1 ||||| 1 ||||| 1  
DB 2 CGAGCGGGTCAAGCTGCTGCTGCAGG 27

#### RESULT 2

BM399411

LOCUS

5009-0-57-E01.t.1 Chilcoat/Turkewitz cDNA (large fraction) EST 17-JAN-2002  
Tetrahymena thermophila cDNA, mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

#### FEATURES

source

1. .30

/organism="Tetrahymena thermophila"

/strain="CU428.1"

/db\_xref="taxon:5911"

/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK-; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

#### BASE COUNT

4 a 10 c 12 g 4 t

#### Query Match

0.5%; Score 18.6; DB 13; Length 30;

Best Local Similarity 84.0%; Pred. No. 5.9e+06;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 719 GCTCAACCTGGGGCTGGTACCC 743

||||| 1 ||||| 1 ||||| 1 ||||| 1

DB 6 GCTACGGCTGGGGCCCGGTACCC 30

#### RESULT 3

AL584657

LOCUS

AL584657 28 bp mRNA linear EST 28-FEB-2001  
DEFINITION AL584657 Stratagene Chick Embryo Lambda cDNA Library (\* 937405)  
Gallus gallus cDNA clone ROS012612, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Al584657

Al584657

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Al584657 28 bp mRNA linear EST 28-FEB-2001  
DEFINITION AL584657 Stratagene Chick Embryo Lambda cDNA Library (\* 937405)  
Gallus gallus cDNA clone ROS012612, mRNA sequence.

Al584657

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REFERENCE
AUTHORS      1 (bases 1 to 29)
              Alonso,J.M., Lelise,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
              ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
              , Zimmerman,J. and Ecker,J.R.
              A Sequence-Indexed Library of Insertion Mutations in the
              Arabidopsis Genome
              Unpublished (2001)
              Contact: Joseph R. Ecker
              Salk Institute Genomic Analysis Laboratory (SIGnAL)
              The Salk Institute for Biological Studies
              10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
              Tel: 858 453 4100 x1752
              Fax: 858 558 6379
              Email: ecker@salk.edu
              This is single pass sequence recovered from the left border of
              TDNA. This sequence lies within an annotated intron of At5g40020.
              Class: TDNA tagged.
FEATURES
source
              1. .29
              /organism="Arabidopsis thaliana"
              /strain="Columbia 0"
              /db_xref="taxon:3702"
              /clone_lib="SALK_067873"
              /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
              each of which contains one or more TDNA insertion
              elements. The resultant fragment for each line was
              directly sequenced to determine the genomic sequence at
              the site of insertion. Details of the protocols used can
              be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT      12 a      3 c      5 g      9 t
ORIGIN
Query Match      0.4%; Score 17; DB 17; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.3e+07;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3464 CACTGGTTATTTATTTATGACTTGA 3488
      |||||  |||  |||||  |||||  |||||
Db 25 CAATGTTAATATCTTTATGACTTGA 1

RESULT 5
Az479681/c
LOCUS
DEFINITION
clone UUGC1M0300G02 R, DNA sequence.
ACCESSION
Az479681
VERSION
Az479681.1 GI:10639845
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0300 row: G column: 02
Seq primer: CACACAGGAACAGCTATGACC

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0017 row: H column: 04
Seq primer: CGTTGTAAACGACGCCGACGT

Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. .26
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC1M0300G02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      13 a      0 c      13 g      0 t
ORIGIN
Query Match      0.4%; Score 16.8; DB 17; Length 26;
Best Local Similarity 90.0%; Pred. No. 1.4e+07;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3110 CTTCTCTCTCTCCACCTCTT 3129
      |||||  |||||  |||||  |||||  |||||
Db 26 CTTCTCTCTCTCTCTCTCTT 7

RESULT 6
Az780072
LOCUS
DEFINITION
2M0017H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0017H04 F, DNA sequence.
ACCESSION
Az780072
VERSION
Az780072.1 GI:12911368
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0017 row: H column: 04
Seq primer: CGTTGTAAACGACGCCGACGT

```

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Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. .26
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC2M0017H04"
/lab_host="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      8 a      6 c      6 g      6 t
ORIGIN
Query Match      0.4%; Score 16.8; DB 17; Length 26;
Best Local Similarity 90.0%; Pred. No. 1.4e+07;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2851 CACATATGCTGCTGGGCATTG 2870
||||||| ||||| |||||
Db 1 CACATATGCTGCTGGGCATTG 20

RESULT 7
AA973948/c
LOCUS      28 bp mRNA linear EST 23-JUL-1998
DEFINITION Oq12d02.s1 NCI_CGAP_G4 Homo sapiens CDNA clone IMAGE:1586115 3' similar to TR:Q35787 Q35787 KINESIN-RELATED PROTEIN. ;, mRNA sequence.
ACCESSION  AA973948.1 GI:3149128
VERSION     AA973948
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 28)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert length: 790 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .28
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1586115"
/lab_host="NCI_CGAP_G4"
/tissue_type="pooled germ cell tumors"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      6 a      3 c      11 g      8 t
ORIGIN
Query Match      0.4%; Score 16.8; DB 9; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.5e+07;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3164 AGCTGCTCCAAAGACATCCAGTATCTCA 3191
||||| ||||| ||||| |||||
Db 28 ACCTCTACATTCATCAGGACCTCA 1

RESULT 8
BM398517
LOCUS      30 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-46-D07.t.1 Chilcoat/Turkewitz CDNA (large fraction) Tetrahymena thermophila CDNA, mRNA sequence.
ACCESSION  BM398517
VERSION     BM398517.1 GI:18198570
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
ORGANISM    Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 30)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1. .30
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz CDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      4 a      10 c      13 g      3 t
ORIGIN
Query Match      0.4%; Score 16.8; DB 13; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.5e+07;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 715 CTCGGCTCAAACCTGGGGCGCTGTACC 742
||||| ||||| ||||| |||||

```









/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gil4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 8 a 3 c 11 g 8 t  
ORIGIN

Query Match 0.4%; Score 16.2; DB 17; Length 30;  
Best Local Similarity 72.4%; Fred. No. 2e+07;  
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2983 TGTCCCATTCATCCTCACCCTACGACTTTG 3011  
||||||| ||||| | || ||  
Db 29 TGTCCCATGCATCCTATCAACCCACCATG 1

Search completed: March 4, 2003, 06:25:19  
Job time : 4732 secs